



SEQUENCE LISTING

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<120> Compositions and Methods of Using Hexokinase V

<130> 016325-008110US

<140> US 10/805,075

<141> 2004-03-19

<150> US 60/456,650

<151> 2003-03-20

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<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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<223> human hexokinase V (HKV, HK5)

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Lys Gly Leu Ala Lys Asp Thr Asn Pro Thr Ala Ala Val Lys Met Leu
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Pro Thr Phe Val Arg Ala Ile Pro Asp Gly Ser Glu Asn Gly Glu Phe
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Leu Ser Leu Asp Leu Gly Gly Ser Lys Phe Arg Val Leu Lys Val Gln
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His Lys Lys Leu Pro Leu Gly Leu Thr Phe Ser Phe Pro Cys Arg Gln
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<212> DNA

<213> Homo sapiens

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<210> 4

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<223> human hexokinase V variant

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Pro Thr Phe Val Arg Ala Ile Pro Asp Gly Ser Glu Asn Gly Glu Phe
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 115 120 125
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Ile	Pro	Leu	Glu	Ile	Met	Gln	Gly	Thr	Gly	Glu	Glu	Leu	Phe	Asp	His	565	570	575	
Ile	Val	Gln	Cys	Ile	Ala	Asp	Phe	Leu	Asp	Tyr	Met	Gly	Leu	Lys	Gly	580	585	590	
Ala	Ser	Leu	Pro	Leu	Gly	Phe	Thr	Phe	Ser	Phe	Pro	Cys	Arg	Gln	Met	595	600	605	
Ser	Ile	Asp	Lys	Gly	Thr	Leu	Ile	Gly	Trp	Thr	Lys	Gly	Phe	Lys	Ala	610	615	620	
Thr	Asp	Cys	Glu	Gly	Glu	Asp	Val	Val	Asp	Met	Leu	Arg	Glu	Ala	Ile	625	630	635	640
Lys	Arg	Arg	Asn	Glu	Phe	Asp	Leu	Asp	Ile	Val	Ala	Val	Val	Asn	Asp	645	650	655	
Thr	Val	Gly	Thr	Met	Met	Thr	Cys	Gly	Tyr	Glu	Asp	Pro	Asn	Cys	Glu	660	665	670	
Ile	Gly	Leu	Ile	Ala	Gly	Thr	Gly	Ser	Asn	Met	Cys	Tyr	Met	Glu	Asp	675	680	685	
Met	Arg	Asn	Ile	Glu	Met	Val	Glu	Gly	Gly	Glu	Gly	Lys	Met	Cys	Ile	690	695	700	
Asn	Thr	Glu	Trp	Gly	Gly	Phe	Gly	Asp	Asn	Gly	Cys	Ile	Asp	Asp	Ile	705	710	715	720

Arg Thr Arg Tyr Asp Thr Glu Val Asp Glu Gly Ser Leu Asn Pro Gly
 725 730 735
 Lys Gln Arg Tyr Glu Lys Met Thr Ser Gly Met Tyr Leu Gly Glu Ile
 740 745 750
 Val Arg Gln Ile Leu Ile Asp Leu Thr Lys Gln Gly Leu Leu Phe Arg
 755 760 765
 Gly Gln Ile Ser Glu Arg Leu Arg Thr Arg Gly Ile Phe Glu Thr Lys
 770 775 780
 Phe Leu Ser Gln Ile Glu Ser Asp Arg Leu Ala Leu Leu Gln Val Arg
 785 790 795 800
 Arg Ile Leu Gln Gln Leu Gly Leu Asp Ser Thr Cys Glu Asp Ser Ile
 805 810 815
 Val Val Lys Glu Val Cys Gly Ala Val Ser Arg Arg Ala Ala Gln Leu
 820 825 830
 Cys Gly Ala Gly Leu Ala Ala Ile Val Glu Lys Arg Arg Glu Asp Gln
 835 840 845
 Gly Leu Glu His Leu Arg Ile Thr Val Gly Val Asp Gly Thr Leu Tyr
 850 855 860
 Lys Leu His Pro His Phe Ser Arg Ile Leu Gln Glu Thr Val Lys Glu
 865 870 875 880
 Leu Ala Pro Arg Cys Asp Val Thr Phe Met Leu Ser Glu Asp Gly Ser
 885 890 895
 Gly Lys Gly Ala Ala Leu Ile Thr Ala Val Ala Lys Arg Leu Gln Gln
 900 905 910
 Ala Gln Lys Glu Asn
 915

<210> 5
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> human hexokinase I (HK1)

<400> 5
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 Asp Gln Val Lys Lys Ile Asp Lys Tyr Leu Tyr Ala Met Arg Leu Ser
 20 25 30
 Asp Glu Thr Leu Ile Asp Ile Met Thr Arg Phe Arg Lys Glu Met Lys
 35 40 45
 Asn Gly Leu Ser Arg Asp Phe Asn Pro Thr Ala Thr Val Lys Met Leu
 50 55 60

Pro	Thr	Phe	Val	Arg	Ser	Ile	Pro	Asp	Gly	Ser	Glu	Lys	Gly	Asp	Phe	65	70	75	80
Ile	Ala	Leu	Asp	Leu	Gly	Gly	Ser	Ser	Phe	Arg	Ile	Leu	Arg	Val	Gln	85	90	95	
Val	Asn	His	Glu	Lys	Asn	Gln	Asn	Val	His	Met	Glu	Ser	Glu	Val	Tyr	100	105	110	
Asp	Thr	Pro	Glu	Asn	Ile	Val	His	Gly	Ser	Gly	Ser	Gln	Leu	Phe	Asp	115	120	125	
His	Val	Ala	Glu	Cys	Leu	Gly	Asp	Phe	Met	Glu	Lys	Arg	Lys	Ile	Lys	130	135	140	
Asp	Lys	Lys	Leu	Pro	Val	Gly	Phe	Thr	Phe	Ser	Phe	Pro	Cys	Gln	Gln	145	150	155	160
Ser	Lys	Ile	Asp	Glu	Ala	Ile	Leu	Ile	Thr	Trp	Thr	Lys	Arg	Phe	Lys	165	170	175	
Ala	Ser	Gly	Val	Glu	Gly	Ala	Asp	Val	Val	Lys	Leu	Leu	Asn	Lys	Ala	180	185	190	
Ile	Lys	Lys	Arg	Gly	Asp	Tyr	Asp	Ala	Asn	Ile	Val	Ala	Val	Val	Asn	195	200	205	
Asp	Thr	Val	Gly	Thr	Met	Met	Thr	Cys	Gly	Tyr	Asp	Asp	Gln	His	Cys	210	215	220	
Glu	Val	Gly	Leu	Ile	Ile	Gly	Thr	Gly	Thr	Asn	Ala	Cys	Tyr	Met	Glu	225	230	235	240
Glu	Leu	Arg	His	Ile	Asp	Leu	Val	Glu	Gly	Asp	Glu	Gly	Arg	Met	Cys	245	250	255	
Ile	Asn	Thr	Glu	Trp	Gly	Ala	Phe	Gly	Asp	Asp	Gly	Ser	Leu	Glu	Asp	260	265	270	
Ile	Arg	Thr	Glu	Phe	Asp	Arg	Glu	Ile	Asp	Arg	Gly	Ser	Leu	Asn	Pro	275	280	285	
Gly	Lys	Gln	Leu	Phe	Glu	Lys	Met	Val	Ser	Gly	Met	Tyr	Leu	Gly	Glu	290	295	300	
Leu	Val	Arg	Leu	Ile	Leu	Val	Lys	Met	Ala	Lys	Glu	Gly	Leu	Leu	Phe	305	310	315	320
Glu	Gly	Arg	Ile	Thr	Pro	Glu	Leu	Leu	Thr	Arg	Gly	Lys	Phe	Asn	Thr	325	330	335	
Ser	Asp	Val	Ser	Ala	Ile	Glu	Lys	Asn	Lys	Glu	Gly	Leu	His	Asn	Ala	340	345	350	
Lys	Glu	Ile	Leu	Thr	Arg	Leu	Gly	Val	Glu	Pro	Ser	Asp	Asp	Asp	Cys	355	360	365	
Val	Ser	Val	Gln	His	Val	Cys	Thr	Ile	Val	Ser	Phe	Arg	Ser	Ala	Asn	370	375	380	

Leu	Val	Ala	Ala	Thr	Leu	Gly	Ala	Ile	Leu	Asn	Arg	Leu	Arg	Asp	Asn	385	390	395	400
Lys	Gly	Thr	Pro	Arg	Leu	Arg	Thr	Thr	Val	Gly	Val	Asp	Gly	Ser	Leu	405	410		415
Tyr	Lys	Thr	His	Pro	Gln	Tyr	Ser	Arg	Arg	Phe	His	Lys	Thr	Leu	Arg	420	425		430
Arg	Leu	Val	Pro	Asp	Ser	Asp	Val	Arg	Phe	Leu	Leu	Ser	Glu	Ser	Gly	435	440		445
Ser	Gly	Lys	Gly	Ala	Ala	Met	Val	Thr	Ala	Val	Ala	Tyr	Arg	Leu	Ala	450	455		460
Glu	Gln	His	Arg	Gln	Ile	Glu	Glu	Thr	Leu	Ala	His	Phe	His	Leu	Thr	465	470		475
Lys	Asp	Met	Leu	Leu	Glu	Val	Lys	Lys	Arg	Met	Arg	Ala	Glu	Met	Glu	485	490		495
Leu	Gly	Leu	Arg	Lys	Gln	Thr	His	Asn	Asn	Ala	Val	Val	Lys	Met	Leu	500	505		510
Pro	Ser	Phe	Val	Arg	Arg	Thr	Pro	Asp	Gly	Thr	Glu	Asn	Gly	Asp	Phe	515	520		525
Leu	Ala	Leu	Asp	Leu	Gly	Gly	Thr	Asn	Phe	Arg	Val	Leu	Leu	Val	Lys	530	535		540
Ile	Arg	Ser	Gly	Lys	Lys	Arg	Thr	Val	Glu	Met	His	Asn	Lys	Ile	Tyr	545	550		555
Ala	Ile	Pro	Ile	Glu	Ile	Met	Gln	Gly	Thr	Gly	Glu	Glu	Leu	Phe	Asp	565	570		575
His	Ile	Val	Ser	Cys	Ile	Ser	Asp	Phe	Leu	Asp	Tyr	Met	Gly	Ile	Lys	580	585		590
Gly	Pro	Arg	Met	Pro	Leu	Gly	Phe	Thr	Phe	Ser	Phe	Pro	Cys	Gln	Gln	595	600		605
Thr	Ser	Leu	Asp	Ala	Gly	Ile	Leu	Ile	Thr	Trp	Thr	Lys	Gly	Phe	Lys	610	615		620
Ala	Thr	Asp	Cys	Val	Gly	His	Asp	Val	Val	Thr	Leu	Leu	Arg	Asp	Ala	625	630		635
Ile	Lys	Arg	Arg	Glu	Glu	Phe	Asp	Leu	Asp	Val	Val	Ala	Val	Val	Asn	645	650		655
Asp	Thr	Val	Gly	Thr	Met	Met	Thr	Cys	Ala	Tyr	Glu	Glu	Pro	Thr	Cys	660	665		670
Glu	Val	Gly	Leu	Ile	Val	Gly	Thr	Gly	Ser	Asn	Ala	Cys	Tyr	Met	Glu	675	680		685
Glu	Met	Lys	Asn	Val	Glu	Met	Val	Glu	Gly	Asp	Gln	Gly	Gln	Met	Cys	690	695		700

Ile Asn Met Glu Trp Gly Ala Phe Gly Asp Asn Gly Cys Leu Asp Asp
 705 710 715 720
 Ile Arg Thr His Tyr Asp Arg Leu Val Asn Glu Tyr Ser Leu Asn Ala
 725 730 735
 Gly Lys Gln Arg Tyr Glu Lys Met Ile Ser Gly Met Tyr Leu Gly Glu
 740 745 750
 Ile Val Arg Asn Ile Leu Ile Asp Phe Thr Lys Lys Gly Phe Leu Phe
 755 760 765
 Arg Gly Gln Ile Ser Glu Thr Met Lys Thr Arg Gly Ile Phe Glu Thr
 770 775 780
 Lys Phe Leu Ser Gln Ile Glu Ser Asp Arg Leu Ala Leu Leu Gln Val
 785 790 795 800
 Arg Ala Ile Leu Gln Gln Leu Gly Leu Asn Ser Thr Cys Asp Asp Ser
 805 810 815
 Ile Leu Val Lys Thr Val Cys Gly Val Val Ser Arg Arg Ala Ala Gln
 820 825 830
 Leu Cys Gly Ala Gly Met Ala Ala Val Val Asp Lys Ile Arg Glu Asn
 835 840 845
 Arg Gly Leu Asp Arg Leu Asn Val Thr Val Gly Val Asp Gly Thr Leu
 850 855 860
 Tyr Lys Leu His Pro His Phe Ser Arg Ile Met His Gln Thr Val Lys
 865 870 875 880
 Glu Leu Ser Pro Lys Cys Asn Val Ser Phe Leu Leu Ser Glu Asp Gly
 885 890 895
 Ser Gly Lys Gly Ala Ala Leu Ile Thr Ala Val Gly Val Arg Leu Arg
 900 905 910
 Thr Glu Ala Ser Ser
 915

<210> 6
 <211> 917
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human hexokinase II (HK2)

<400> 6
 Met Ile Ala Ser His Leu Leu Ala Tyr Phe Phe Thr Glu Leu Asn His
 1 5 10 15
 Asp Gln Val Gln Lys Val Asp Gln Tyr Leu Tyr His Met Arg Leu Ser
 20 25 30
 Asp Glu Thr Leu Leu Glu Ile Ser Lys Arg Phe Arg Lys Glu Met Glu
 35 40 45

Lys	Gly	Leu	Gly	Ala	Thr	Thr	His	Pro	Thr	Ala	Ala	Val	Lys	Met	Leu	50	55	60
Pro	Thr	Phe	Val	Arg	Ser	Thr	Pro	Asp	Gly	Thr	Glu	His	Gly	Glu	Phe	65	70	75
Leu	Ala	Leu	Asp	Leu	Gly	Gly	Thr	Asn	Phe	Arg	Val	Leu	Trp	Val	Lys	85	90	95
Val	Thr	Asp	Asn	Gly	Leu	Gln	Lys	Val	Glu	Met	Glu	Asn	Gln	Ile	Tyr	100	105	110
Ala	Ile	Pro	Glu	Asp	Ile	Met	Arg	Gly	Ser	Gly	Thr	Gln	Leu	Phe	Asp	115	120	125
His	Ile	Ala	Glu	Cys	Leu	Ala	Asn	Phe	Met	Asp	Lys	Leu	Gln	Ile	Lys	130	135	140
Asp	Lys	Lys	Leu	Pro	Leu	Gly	Phe	Thr	Phe	Ser	Phe	Pro	Cys	His	Gln	145	150	155
Thr	Lys	Leu	Asp	Glu	Ser	Phe	Leu	Val	Ser	Trp	Thr	Lys	Gly	Phe	Lys	165	170	175
Ser	Ser	Gly	Val	Glu	Gly	Arg	Asp	Val	Val	Ala	Leu	Ile	Arg	Lys	Ala	180	185	190
Ile	Gln	Arg	Arg	Gly	Asp	Phe	Asp	Ile	Asp	Ile	Val	Ala	Val	Val	Asn	195	200	205
Asp	Thr	Val	Gly	Thr	Met	Met	Thr	Cys	Gly	Tyr	Asp	Asp	His	Asn	Cys	210	215	220
Glu	Ile	Gly	Leu	Ile	Val	Gly	Thr	Gly	Ser	Asn	Ala	Cys	Tyr	Met	Glu	225	230	235
Glu	Met	Arg	His	Ile	Asp	Met	Val	Glu	Gly	Asp	Glu	Gly	Arg	Met	Cys	245	250	255
Ile	Asn	Met	Glu	Trp	Gly	Ala	Phe	Gly	Asp	Asp	Gly	Ser	Leu	Asn	Asp	260	265	270
Ile	Arg	Thr	Glu	Phe	Asp	Gln	Glu	Ile	Asp	Met	Gly	Ser	Leu	Asn	Pro	275	280	285
Gly	Lys	Gln	Leu	Phe	Glu	Lys	Met	Ile	Ser	Gly	Met	Tyr	Met	Gly	Glu	290	295	300
Leu	Val	Arg	Leu	Ile	Leu	Val	Lys	Met	Ala	Lys	Glu	Glu	Leu	Leu	Phe	305	310	315
Gly	Gly	Lys	Leu	Ser	Pro	Glu	Leu	Leu	Asn	Thr	Gly	Arg	Phe	Glu	Thr	325	330	335
Lys	Asp	Ile	Ser	Asp	Ile	Glu	Gly	Glu	Lys	Asp	Gly	Ile	Arg	Lys	Ala	340	345	350
Arg	Glu	Val	Leu	Met	Arg	Leu	Gly	Leu	Asp	Pro	Thr	Gln	Glu	Asp	Cys	355	360	365

Val	Ala	Thr	His	Arg	Ile	Cys	Gln	Ile	Val	Ser	Thr	Arg	Ser	Ala	Ser	370	375	380
Leu	Cys	Ala	Ala	Thr	Leu	Ala	Ala	Val	Leu	Gln	Arg	Ile	Lys	Glu	Asn	385	390	395
Lys	Gly	Glu	Glu	Arg	Leu	Arg	Ser	Thr	Ile	Gly	Val	Asp	Gly	Ser	Val	405	410	415
Tyr	Lys	Lys	His	Pro	His	Phe	Ala	Lys	Arg	Leu	His	Lys	Thr	Val	Arg	420	425	430
Arg	Leu	Val	Pro	Gly	Cys	Asp	Val	Arg	Phe	Leu	Arg	Ser	Glu	Asp	Gly	435	440	445
Ser	Gly	Lys	Gly	Ala	Ala	Met	Val	Thr	Ala	Val	Ala	Tyr	Arg	Leu	Ala	450	455	460
Asp	Gln	His	Arg	Ala	Arg	Gln	Lys	Thr	Leu	Glu	His	Leu	Gln	Leu	Ser	465	470	475
His	Asp	Gln	Leu	Leu	Glu	Val	Lys	Arg	Arg	Met	Lys	Val	Glu	Met	Glu	485	490	495
Arg	Gly	Leu	Ser	Lys	Glu	Thr	His	Ala	Ser	Ala	Pro	Val	Lys	Met	Leu	500	505	510
Pro	Thr	Tyr	Val	Cys	Ala	Thr	Pro	Asp	Gly	Thr	Glu	Lys	Gly	Asp	Phe	515	520	525
Leu	Ala	Leu	Asp	Leu	Gly	Gly	Thr	Asn	Phe	Arg	Val	Leu	Leu	Val	Arg	530	535	540
Val	Arg	Asn	Gly	Lys	Trp	Gly	Gly	Val	Glu	Met	His	Asn	Lys	Ile	Tyr	545	550	555
Ala	Ile	Pro	Gln	Glu	Val	Met	His	Gly	Thr	Gly	Asp	Glu	Leu	Phe	Asp	565	570	575
His	Ile	Val	Gln	Cys	Ile	Ala	Asp	Phe	Leu	Glu	Tyr	Met	Gly	Met	Lys	580	585	590
Gly	Val	Ser	Leu	Pro	Leu	Gly	Phe	Thr	Phe	Ser	Phe	Pro	Cys	Gln	Gln	595	600	605
Asn	Ser	Leu	Asp	Glu	Ser	Ile	Leu	Leu	Lys	Trp	Thr	Lys	Gly	Phe	Lys	610	615	620
Ala	Ser	Gly	Cys	Glu	Gly	Glu	Asp	Val	Val	Thr	Leu	Leu	Lys	Glu	Ala	625	630	635
Ile	His	Arg	Arg	Glu	Glu	Phe	Asp	Leu	Asp	Val	Val	Ala	Val	Val	Asn	645	650	655
Asp	Thr	Val	Gly	Thr	Met	Met	Thr	Cys	Gly	Phe	Glu	Asp	Pro	His	Cys	660	665	670
Glu	Val	Gly	Leu	Ile	Val	Gly	Thr	Gly	Ser	Asn	Ala	Cys	Tyr	Met	Glu	675	680	685

Glu Met Arg Asn Val Glu Leu Val Glu Gly Glu Glu Gly Arg Met Cys
 690 695 700
 Val Asn Met Glu Trp Gly Ala Phe Gly Asp Asn Gly Cys Leu Asp Asp
 705 710 715 720
 Phe Arg Thr Glu Phe Asp Val Ala Val Asp Glu Leu Ser Leu Asn Pro
 725 730 735
 Gly Lys Gln Arg Phe Glu Lys Met Ile Ser Gly Met Tyr Leu Gly Glu
 740 745 750
 Ile Val Arg Asn Ile Leu Ile Asp Phe Thr Lys Arg Gly Leu Leu Phe
 755 760 765
 Arg Gly Arg Ile Ser Glu Arg Leu Lys Thr Arg Gly Ile Phe Glu Thr
 770 775 780
 Lys Phe Leu Ser Gln Ile Glu Ser Asp Cys Leu Ala Leu Leu Gln Val
 785 790 795 800
 Arg Ala Ile Leu Gln His Leu Gly Leu Glu Ser Thr Cys Asp Asp Ser
 805 810 815
 Ile Ile Val Lys Glu Val Cys Thr Val Val Ala Arg Arg Ala Ala Gln
 820 825 830
 Leu Cys Gly Ala Gly Met Ala Ala Val Val Asp Arg Ile Arg Glu Asn
 835 840 845
 Arg Gly Leu Asp Ala Leu Lys Val Thr Val Gly Val Asp Gly Thr Leu
 850 855 860
 Tyr Lys Leu His Pro His Phe Ala Lys Val Met His Glu Thr Val Lys
 865 870 875 880
 Asp Leu Ala Pro Lys Cys Asp Val Ser Phe Leu Gln Ser Glu Asp Gly
 885 890 895
 Ser Gly Lys Gly Ala Ala Leu Ile Thr Ala Val Ala Cys Arg Ile Arg
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 Glu Ala Gly Gln Arg
 915

<210> 7

<211> 923

<212> PRT

<213> Homo sapiens

<220>

<223> human hexokinase III (HK3)

<400> 7

Met Asp Ser Ile Gly Ser Ser Gly Leu Arg Gln Gly Glu Glu Thr Leu
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 Ser Cys Ser Glu Glu Gly Leu Pro Gly Pro Ser Asp Ser Ser Glu Leu
 20 25 30

Val	Gln	Glu	Cys	Leu	Gln	Gln	Phe	Lys	Val	Thr	Arg	Ala	Gln	Leu	Gln			
		35					40					45						
Gln	Ile	Gln	Ala	Ser	Leu	Leu	Gly	Ser	Met	Glu	Gln	Ala	Leu	Arg	Gly			
	50					55					60							
Gln	Ala	Ser	Pro	Ala	Pro	Ala	Val	Arg	Met	Leu	Pro	Thr	Tyr	Val	Gly			
	65				70					75					80			
Ser	Thr	Pro	His	Gly	Thr	Glu	Gln	Gly	Asp	Phe	Val	Val	Leu	Glu	Leu			
				85					90					95				
Gly	Ala	Thr	Gly	Ala	Ser	Leu	Arg	Val	Leu	Trp	Val	Thr	Leu	Thr	Gly			
			100					105					110					
Ile	Glu	Gly	His	Arg	Val	Glu	Pro	Arg	Ser	Gln	Glu	Phe	Val	Ile	Pro			
	115						120					125						
Gln	Glu	Val	Met	Leu	Gly	Ala	Gly	Gln	Gln	Leu	Phe	Asp	Phe	Ala	Ala			
	130					135					140							
His	Cys	Leu	Ser	Glu	Phe	Leu	Asp	Ala	Gln	Pro	Val	Asn	Lys	Gln	Gly			
	145				150					155					160			
Leu	Gln	Leu	Gly	Phe	Ser	Phe	Ser	Phe	Pro	Cys	His	Gln	Thr	Gly	Leu			
				165					170					175				
Asp	Arg	Ser	Thr	Leu	Ile	Ser	Trp	Thr	Lys	Gly	Phe	Arg	Cys	Ser	Gly			
			180					185					190					
Val	Glu	Gly	Gln	Asp	Val	Val	Gln	Leu	Leu	Arg	Asp	Ala	Ile	Arg	Arg			
		195					200					205						
Gln	Gly	Ala	Tyr	Asn	Ile	Asp	Val	Val	Ala	Val	Val	Asn	Asp	Thr	Val			
	210					215						220						
Gly	Thr	Met	Met	Gly	Cys	Glu	Pro	Gly	Val	Arg	Pro	Cys	Glu	Val	Gly			
	225				230					235					240			
Leu	Val	Val	Asp	Thr	Gly	Thr	Asn	Ala	Cys	Tyr	Met	Glu	Glu	Ala	Arg			
				245					250					255				
His	Val	Ala	Val	Leu	Asp	Glu	Asp	Arg	Gly	Arg	Val	Cys	Val	Ser	Val			
			260					265					270					
Glu	Trp	Gly	Ser	Leu	Ser	Asp	Asp	Gly	Ala	Leu	Gly	Pro	Val	Leu	Thr			
		275					280					285						
Thr	Phe	Asp	His	Thr	Leu	Asp	His	Glu	Ser	Leu	Asn	Pro	Gly	Ala	Gln			
	290					295					300							
Arg	Phe	Glu	Lys	Met	Ile	Gly	Gly	Leu	Tyr	Leu	Gly	Glu	Leu	Val	Arg			
	305				310					315					320			
Leu	Val	Leu	Ala	His	Leu	Ala	Arg	Cys	Gly	Val	Leu	Phe	Gly	Gly	Cys			
				325					330					335				
Thr	Ser	Pro	Ala	Leu	Leu	Ser	Gln	Gly	Ser	Ile	Leu	Leu	Glu	His	Val			
			340					345					350					

Ala	Glu	Met	Glu	Asp	Pro	Ser	Thr	Gly	Ala	Ala	Arg	Val	His	Ala	Ile	355	360	365
Leu	Gln	Asp	Leu	Gly	Leu	Ser	Pro	Gly	Ala	Ser	Asp	Val	Glu	Leu	Val	370	375	380
Gln	His	Val	Cys	Ala	Ala	Val	Cys	Thr	Arg	Ala	Ala	Gln	Leu	Cys	Ala	385	390	395
Ala	Ala	Leu	Ala	Ala	Val	Leu	Ser	Cys	Leu	Gln	His	Ser	Arg	Glu	Gln	405	410	415
Gln	Thr	Leu	Gln	Val	Ala	Val	Ala	Thr	Gly	Gly	Arg	Val	Cys	Glu	Arg	420	425	430
His	Pro	Arg	Phe	Cys	Ser	Val	Leu	Gln	Gly	Thr	Val	Met	Leu	Leu	Ala	435	440	445
Pro	Glu	Cys	Asp	Val	Ser	Leu	Ile	Pro	Ser	Val	Asp	Gly	Gly	Gly	Arg	450	455	460
Gly	Val	Ala	Met	Val	Thr	Ala	Val	Ala	Ala	Arg	Leu	Ala	Ala	His	Arg	465	470	475
Arg	Leu	Leu	Glu	Glu	Thr	Leu	Ala	Pro	Phe	Arg	Leu	Asn	His	Asp	Gln	485	490	495
Leu	Ala	Ala	Val	Gln	Ala	Gln	Met	Arg	Lys	Ala	Met	Ala	Lys	Gly	Leu	500	505	510
Arg	Gly	Glu	Ala	Ser	Ser	Leu	Arg	Met	Leu	Pro	Thr	Phe	Val	Arg	Ala	515	520	525
Thr	Pro	Asp	Gly	Ser	Glu	Arg	Gly	Asp	Phe	Leu	Ala	Leu	Asp	Leu	Gly	530	535	540
Gly	Thr	Asn	Phe	Arg	Val	Leu	Leu	Val	Arg	Val	Thr	Thr	Gly	Val	Gln	545	550	555
Ile	Thr	Ser	Glu	Ile	Tyr	Ser	Ile	Pro	Glu	Thr	Val	Ala	Gln	Gly	Ser	565	570	575
Gly	Gln	Gln	Leu	Phe	Asp	His	Ile	Val	Asp	Cys	Ile	Val	Asp	Phe	Gln	580	585	590
Gln	Lys	Gln	Gly	Leu	Ser	Gly	Gln	Ser	Leu	Pro	Leu	Gly	Phe	Thr	Phe	595	600	605
Ser	Phe	Pro	Cys	Arg	Gln	Leu	Gly	Leu	Asp	Gln	Gly	Ile	Leu	Leu	Asn	610	615	620
Trp	Thr	Lys	Gly	Phe	Lys	Ala	Ser	Asp	Cys	Glu	Gly	Gln	Asp	Val	Val	625	630	635
Ser	Leu	Leu	Arg	Glu	Ala	Ile	Thr	Arg	Arg	Gln	Ala	Val	Glu	Leu	Asn	645	650	655
Val	Val	Ala	Ile	Val	Asn	Asp	Thr	Val	Gly	Thr	Met	Met	Ser	Cys	Gly	660	665	670

Tyr Glu Asp Pro Arg Cys Glu Ile Gly Leu Ile Val Gly Thr Gly Thr
 675 680 685
 Asn Ala Cys Tyr Met Glu Glu Leu Arg Asn Val Ala Gly Val Pro Gly
 690 695 700
 Asp Ser Gly Arg Met Cys Ile Asn Met Glu Trp Gly Ala Phe Gly Asp
 705 710 715 720
 Asp Gly Ser Leu Ala Met Leu Ser Thr Arg Phe Asp Ala Ser Val Asp
 725 730 735
 Gln Ala Ser Ile Asn Pro Gly Lys Gln Arg Phe Glu Lys Met Ile Ser
 740 745 750
 Gly Met Tyr Leu Gly Glu Ile Val Arg His Ile Leu Leu His Leu Thr
 755 760 765
 Ser Leu Gly Val Leu Phe Arg Gly Gln Gln Ile Gln Arg Leu Gln Thr
 770 775 780
 Arg Asp Ile Phe Lys Thr Lys Phe Leu Ser Glu Ile Glu Ser Asp Ser
 785 790 795 800
 Leu Ala Leu Arg Gln Val Arg Ala Ile Leu Glu Asp Leu Gly Leu Pro
 805 810 815
 Leu Thr Ser Asp Asp Ala Leu Met Val Leu Glu Val Cys Gln Ala Val
 820 825 830
 Ser Gln Arg Ala Ala Gln Leu Cys Gly Ala Gly Val Ala Ala Val Val
 835 840 845
 Glu Lys Ile Arg Gly Asn Arg Gly Leu Glu Glu Leu Ala Val Ser Val
 850 855 860
 Gly Val Asp Gly Thr Leu Tyr Lys Leu His Pro Arg Phe Ser Ser Leu
 865 870 875 880
 Val Ala Ala Thr Val Arg Glu Leu Ala Pro Arg Cys Val Val Thr Phe
 885 890 895
 Leu Gln Ser Glu Asp Gly Ser Gly Lys Gly Ala Ala Leu Val Thr Ala
 900 905 910
 Val Ala Cys Arg Leu Ala Gln Leu Thr Arg Val
 915 920

<210> 8
 <211> 465
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human hexokinase IV (HK4p)

<400> 8
 Met Leu Asp Asp Arg Ala Arg Met Glu Ala Ala Lys Lys Glu Lys Val
 1 5 10 15

Glu	Gln	Ile	Leu	Ala	Glu	Phe	Gln	Leu	Gln	Glu	Glu	Asp	Leu	Lys	Lys	20	25	30	
Val	Met	Arg	Arg	Met	Gln	Lys	Glu	Met	Asp	Arg	Gly	Leu	Arg	Leu	Glu	35	40	45	
Thr	His	Glu	Glu	Ala	Ser	Val	Lys	Met	Leu	Pro	Thr	Tyr	Val	Arg	Ser	50	55	60	
Thr	Pro	Glu	Gly	Ser	Glu	Val	Gly	Asp	Phe	Leu	Ser	Leu	Asp	Leu	Gly	65	70	75	80
Gly	Thr	Asn	Phe	Arg	Val	Met	Leu	Val	Lys	Val	Gly	Glu	Gly	Glu	Glu	85	90	95	
Gly	Gln	Trp	Ser	Val	Lys	Thr	Lys	His	Gln	Met	Tyr	Ser	Ile	Pro	Glu	100	105	110	
Asp	Ala	Met	Thr	Gly	Thr	Ala	Glu	Met	Leu	Phe	Asp	Tyr	Ile	Ser	Glu	115	120	125	
Cys	Ile	Ser	Asp	Phe	Leu	Asp	Lys	His	Gln	Met	Lys	His	Lys	Lys	Leu	130	135	140	
Pro	Leu	Gly	Phe	Thr	Phe	Ser	Phe	Pro	Val	Arg	His	Glu	Asp	Ile	Asp	145	150	155	160
Lys	Gly	Ile	Leu	Leu	Asn	Trp	Thr	Lys	Gly	Phe	Lys	Ala	Ser	Gly	Ala	165	170	175	
Glu	Gly	Asn	Asn	Val	Val	Gly	Leu	Leu	Arg	Asp	Ala	Ile	Lys	Arg	Arg	180	185	190	
Gly	Asp	Phe	Glu	Met	Asp	Val	Val	Ala	Met	Val	Asn	Asp	Thr	Val	Ala	195	200	205	
Thr	Met	Ile	Ser	Cys	Tyr	Tyr	Glu	Asp	His	Gln	Cys	Glu	Val	Gly	Met	210	215	220	
Ile	Val	Gly	Thr	Gly	Cys	Asn	Ala	Cys	Tyr	Met	Glu	Glu	Met	Gln	Asn	225	230	235	240
Val	Glu	Leu	Val	Glu	Gly	Asp	Glu	Gly	Arg	Met	Cys	Val	Asn	Thr	Glu	245	250	255	
Trp	Gly	Ala	Phe	Gly	Asp	Ser	Gly	Glu	Leu	Asp	Glu	Phe	Leu	Leu	Glu	260	265	270	
Tyr	Asp	Arg	Leu	Val	Asp	Glu	Ser	Ser	Ala	Asn	Pro	Gly	Gln	Gln	Leu	275	280	285	
Tyr	Glu	Lys	Leu	Ile	Gly	Gly	Lys	Tyr	Met	Gly	Glu	Leu	Val	Arg	Leu	290	295	300	
Val	Leu	Leu	Arg	Leu	Val	Asp	Glu	Asn	Leu	Leu	Phe	His	Gly	Glu	Ala	305	310	315	320
Ser	Glu	Gln	Leu	Arg	Thr	Arg	Gly	Ala	Phe	Glu	Thr	Arg	Phe	Val	Ser	325	330	335	

Gln Val Glu Ser Asp Thr Gly Asp Arg Lys Gln Ile Tyr Asn Ile Leu
 340 345 350
 Ser Thr Leu Gly Leu Arg Pro Ser Thr Thr Asp Cys Asp Ile Val Arg
 355 360 365
 Arg Ala Cys Glu Ser Val Ser Thr Arg Ala Ala His Met Cys Ser Ala
 370 375 380
 Gly Leu Ala Gly Val Ile Asn Arg Met Arg Glu Ser Arg Ser Glu Asp
 385 390 395 400
 Val Met Arg Ile Thr Val Gly Val Asp Gly Ser Val Tyr Lys Leu His
 405 410 415
 Pro Ser Phe Lys Glu Arg Phe His Ala Ser Val Arg Arg Leu Thr Pro
 420 425 430
 Ser Cys Glu Ile Thr Phe Ile Glu Ser Glu Glu Gly Ser Gly Arg Gly
 435 440 445
 Ala Ala Leu Val Ser Ala Val Ala Cys Lys Lys Ala Cys Met Leu Gly
 450 455 460
 Gln
 465

<210> 9
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hexahistidine
 affinity tag

<400> 9
 His His His His His His
 1 5

<210> 10
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:poly-Gly
 flexible linker

<220>
 <221> MOD_RES
 <222> (6)..(200)
 <223> Gly residues from position 6 to 200 may be present
 or absent

<400> 10
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 35 40 45
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 50 55 60
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 65 70 75 80
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 85 90 95
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 100 105 110
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 115 120 125
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 145 150 155 160
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 165 170 175
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 180 185 190
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 195 200

<210> 11
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific primer HKI forward

<400> 11
 gctggagatg gaaaatcaca ccacc

25

<210> 12
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific primer HKI reverse

<400> 12
 cccccacga gacaaacaga atg

23

<210> 13
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific primer HKII forward

 <400> 13
 gggaagggg agtttttagt ttgttttac 29

 <210> 14
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific primer HKII reverse

 <400> 14
 ccacaggcga atgaggtatt tctatgac 28

 <210> 15
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific primer HKIII forward

 <400> 15
 ttgcggcagg gggaagaaac 20

 <210> 16
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific primer HKIII reverse

 <400> 16
 caccacgaag tctccttgct cagtg 25

 <210> 17
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific primer HKIV forward

<400> 17
 ctgagtggct tgtgattctg ggatg 25

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific primer HKIV reverse

<400> 18
 ctgcttgggg tttcttcctg agc 23

<210> 19
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific primer HKV forward

<400> 19
 ctatggcttt cagtcttgtg gctgc 25

<210> 20
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific primer HKV reverse

<400> 20
 agtgctccct ggcaatcaac ctc 23

<210> 21
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific positive control primer Human GAPDH
 forward

<400> 21
 gagaaggctg gggctcatTT gc 22

<210> 22
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:RT-PCR
 gene-specific positive control primer Human GAPDH
 reverse

<400> 22
 tgtcgctggt gaagtcagag gagacc 26

<210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:quantitative
 real-time PCR gene-specific primer mHK5 (sense)

<400> 23
 ctgcaggaga cggtgaaaga g 21

<210> 24
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:quantitative
 real-time PCR gene-specific primer mHK5
 (antisense)

<400> 24
 cgctgccgtc ttctgaca 18

<210> 25
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:endogenous
 control mouse beta-actin primer (sense)

<400> 25
 cgtgaaaaga tgaccagat ca 22

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:endogenous
 control mouse beta-actin primer (antisense)

<400> 26
 cacagcctgg atggctacgt 20